

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2007; month=11; day=28; hr=9; min=55; sec=58; ms=674;]

=====

Application No: 10579090 Version No: 1.0

Input Set:

Output Set:

Started: 2007-11-07 15:28:37.874
Finished: 2007-11-07 15:28:40.427
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 553 ms
Total Warnings: 18
Total Errors: 0
No. of SeqIDs Defined: 18
Actual SeqID Count: 18

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 402	Undefined organism found in <213> in SEQ ID (5)
W 402	Undefined organism found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 402	Undefined organism found in <213> in SEQ ID (8)
W 402	Undefined organism found in <213> in SEQ ID (9)
W 402	Undefined organism found in <213> in SEQ ID (10)
W 402	Undefined organism found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 402	Undefined organism found in <213> in SEQ ID (14)
W 402	Undefined organism found in <213> in SEQ ID (15)
W 402	Undefined organism found in <213> in SEQ ID (16)
W 402	Undefined organism found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (18)

SEQUENCE LISTING

<110> UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC.

<120> DNA SEQUENCE AND EXPRESSED RECOMBINANT GLYCOPROTEINS
RELATED TO FELINE THYROTROPIN

<130> 235-00540201

<140> 10579090

<141> 2007-11-07

<150> PCT/US04/03779

<151> 2004-11-12

<150> 60/534,205

<151> 2004-01-05

<150> 60/519,302

<151> 2003-11-12

<160> 18

<170> PatentIn Ver. 3.3

<210> 1

<211> 118

<212> PRT

<213> Felis sp.

<400> 1

Phe	Cys	Phe	Pro	Thr	Glu	Tyr	Met	Met	His	Val	Glu	Arg	Lys	Glu	Cys
1				5					10					15	

Ala	Tyr	Cys	Leu	Thr	Ile	Asn	Thr	Thr	Ile	Cys	Ala	Gly	Tyr	Cys	Met
			20					25					30		

Thr	Arg	Asp	Ile	Asn	Gly	Lys	Leu	Phe	Leu	Pro	Lys	Tyr	Ala	Leu	Ser
		35					40					45			

Gln	Asp	Val	Cys	Thr	Tyr	Arg	Asp	Phe	Leu	Tyr	Lys	Thr	Val	Glu	Ile
	50					55					60				

Pro	Gly	Cys	Pro	His	His	Val	Thr	Pro	Tyr	Phe	Ser	Tyr	Pro	Val	Ala
65					70					75				80	

Val	Ser	Cys	Lys	Cys	Gly	Lys	Cys	Asn	Thr	Asp	Tyr	Ser	Asp	Cys	Ile
			85					90						95	

His	Glu	Ala	Ile	Lys	Thr	Asn	Asp	Cys	Thr	Lys	Pro	Gln	Lys	Ser	Asp
		100						105					110		

Val	Val	Gly	Val	Ser	Ile
					115

<210> 2

<211> 138

<212> PRT

<213> Felis sp.

<400> 2

Met Thr Ala Ile Tyr Leu Met Ser Val Leu Phe Gly Leu Ala Cys Gly
1 5 10 15

Gln Ala Met Ser Phe Cys Phe Pro Thr Glu Tyr Met Met His Val Glu
20 25 30

Arg Lys Glu Cys Ala Tyr Cys Leu Thr Ile Asn Thr Thr Ile Cys Ala
35 40 45

Gly Tyr Cys Met Thr Arg Asp Ile Asn Gly Lys Leu Phe Leu Pro Lys
50 55 60

Tyr Ala Leu Ser Gln Asp Val Cys Thr Tyr Arg Asp Phe Leu Tyr Lys
65 70 75 80

Thr Val Glu Ile Pro Gly Cys Pro His His Val Thr Pro Tyr Phe Ser
85 90 95

Tyr Pro Val Ala Val Ser Cys Lys Cys Gly Lys Cys Asn Thr Asp Tyr
100 105 110

Ser Asp Cys Ile His Glu Ala Ile Lys Thr Asn Asp Cys Thr Lys Pro
115 120 125

Gln Lys Ser Asp Val Val Gly Val Ser Ile
130 135

<210> 3

<211> 96

<212> PRT

<213> Felis sp.

<400> 3

Phe Pro Asp Gly Glu Phe Thr Met Gln Gly Cys Pro Glu Cys Lys Leu
1 5 10 15

Lys Glu Asn Lys Tyr Phe Ser Lys Leu Gly Ala Pro Ile Tyr Gln Cys
20 25 30

Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro Ala Arg Ser Lys
35 40 45

Lys Thr Met Leu Val Pro Lys Asn Ile Thr Ser Glu Ala Thr Cys Cys
50 55 60

Val Ala Lys Ala Phe Thr Lys Ala Thr Val Met Gly Asn Ala Lys Val
65 70 75 80

Glu Asn His Thr Glu Cys His Cys Ser Thr Cys Tyr His His Lys Ile
85 90 95

<210> 4
<211> 120
<212> PRT
<213> Felis sp.

<400> 4

Met	Asp	Tyr	Tyr	Arg	Lys	Tyr	Ala	Ala	Val	Ile	Leu	Ala	Ile	Leu	Ser
1				5					10					15	
Val	Phe	Leu	His	Ile	Leu	His	Ser	Phe	Pro	Asp	Gly	Glu	Phe	Thr	Met
			20					25					30		
Gln	Gly	Cys	Pro	Glu	Cys	Lys	Leu	Lys	Glu	Asn	Lys	Tyr	Phe	Ser	Lys
		35					40					45			
Leu	Gly	Ala	Pro	Ile	Tyr	Gln	Cys	Met	Gly	Cys	Cys	Phe	Ser	Arg	Ala
	50					55					60				
Tyr	Pro	Thr	Pro	Ala	Arg	Ser	Lys	Lys	Thr	Met	Leu	Val	Pro	Lys	Asn
65					70				75						80
Ile	Thr	Ser	Glu	Ala	Thr	Cys	Cys	Val	Ala	Lys	Ala	Phe	Thr	Lys	Ala
				85					90					95	
Thr	Val	Met	Gly	Asn	Ala	Lys	Val	Glu	Asn	His	Thr	Glu	Cys	His	Cys
		100						105					110		
Ser	Thr	Cys	Tyr	His	His	Lys	Ile								
		115					120								

<210> 5
<211> 244
<212> PRT
<213> Felis sp.

<400> 5

Phe	Cys	Phe	Pro	Thr	Glu	Tyr	Met	Met	His	Val	Glu	Arg	Lys	Glu	Cys
1				5					10					15	
Ala	Tyr	Cys	Leu	Thr	Ile	Asn	Thr	Thr	Ile	Cys	Ala	Gly	Tyr	Cys	Met
			20					25					30		
Thr	Arg	Asp	Ile	Asn	Gly	Lys	Leu	Phe	Leu	Pro	Lys	Tyr	Ala	Leu	Ser
		35					40					45			
Gln	Asp	Val	Cys	Thr	Tyr	Arg	Asp	Phe	Leu	Tyr	Lys	Thr	Val	Glu	Ile
	50					55					60				
Pro	Gly	Cys	Pro	His	His	Val	Thr	Pro	Tyr	Phe	Ser	Tyr	Pro	Val	Ala
65					70				75						80
Val	Ser	Cys	Lys	Cys	Gly	Lys	Cys	Asn	Thr	Asp	Tyr	Ser	Asp	Cys	Ile
				85					90					95	
His	Glu	Ala	Ile	Lys	Thr	Asn	Asp	Cys	Thr	Lys	Pro	Gln	Lys	Ser	Asp
		100						105					110		

Val Val Gly Val Ser Ile Gln Asp Ser Ser Ser Ser Lys Ala Pro Ser
115 120 125

Ala Ser Leu Pro Ser Pro Thr Arg Leu Pro Gly Pro Ser Asp Thr Pro
130 135 140

Ile Leu Pro Gln Phe Pro Asp Gly Glu Phe Thr Met Gln Gly Cys Pro
145 150 155 160

Glu Cys Lys Leu Lys Glu Asn Lys Tyr Phe Ser Lys Leu Gly Ala Pro
165 170 175

Ile Tyr Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro
180 185 190

Ala Arg Ser Lys Lys Thr Met Leu Val Pro Lys Asn Ile Thr Ser Glu
195 200 205

Ala Thr Cys Cys Val Ala Lys Ala Phe Thr Lys Ala Thr Val Met Gly
210 215 220

Asn Ala Lys Val Glu Asn His Thr Glu Cys His Cys Ser Thr Cys Tyr
225 230 235 240

His His Lys Ile

<210> 6

<211> 264

<212> PRT

<213> Felis sp.

<400> 6

Met Thr Ala Ile Tyr Leu Met Ser Val Leu Phe Gly Leu Ala Cys Gly
1 5 10 15

Gln Ala Met Ser Phe Cys Phe Pro Thr Glu Tyr Met Met His Val Glu
20 25 30

Arg Lys Glu Cys Ala Tyr Cys Leu Thr Ile Asn Thr Thr Ile Cys Ala
35 40 45

Gly Tyr Cys Met Thr Arg Asp Ile Asn Gly Lys Leu Phe Leu Pro Lys
50 55 60

Tyr Ala Leu Ser Gln Asp Val Cys Thr Tyr Arg Asp Phe Leu Tyr Lys
65 70 75 80

Thr Val Glu Ile Pro Gly Cys Pro His His Val Thr Pro Tyr Phe Ser
85 90 95

Tyr Pro Val Ala Val Ser Cys Lys Cys Gly Lys Cys Asn Thr Asp Tyr
100 105 110

Ser Asp Cys Ile His Glu Ala Ile Lys Thr Asn Asp Cys Thr Lys Pro
115 120 125

Gln Lys Ser Asp Val Val Gly Val Ser Ile Gln Asp Ser Ser Ser Ser
 130 135 140

Lys Ala Pro Ser Ala Ser Leu Pro Ser Pro Thr Arg Leu Pro Gly Pro
 145 150 155 160

Ser Asp Thr Pro Ile Leu Pro Gln Phe Pro Asp Gly Glu Phe Thr Met
 165 170 175

Gln Gly Cys Pro Glu Cys Lys Leu Lys Glu Asn Lys Tyr Phe Ser Lys
 180 185 190

Leu Gly Ala Pro Ile Tyr Gln Cys Met Gly Cys Cys Phe Ser Arg Ala
 195 200 205

Tyr Pro Thr Pro Ala Arg Ser Lys Lys Thr Met Leu Val Pro Lys Asn
 210 215 220

Ile Thr Ser Glu Ala Thr Cys Cys Val Ala Lys Ala Phe Thr Lys Ala
 225 230 235 240

Thr Val Met Gly Asn Ala Lys Val Glu Asn His Thr Glu Cys His Cys
 245 250 255

Ser Thr Cys Tyr His His Lys Ile
 260

<210> 7
 <211> 417
 <212> DNA
 <213> Felis sp.

<220>
 <221> CDS
 <222> (1)..(414)
 <223> coding region for SEQ ID NO: 2

<220>
 <221> CDS
 <222> (61)..(414)
 <223> coding region for SEQ ID NO: 1

<400> 7
 atg act gct atc tac ctg atg tcc gtg ctt ttt ggc ctg gca tgt gga 48
 Met Thr Ala Ile Tyr Leu Met Ser Val Leu Phe Gly Leu Ala Cys Gly
 1 5 10 15

caa gcg atg tct ttt tgt ttt cca act gag tat atg atg cat gtc gaa 96
 Gln Ala Met Ser Phe Cys Phe Pro Thr Glu Tyr Met Met His Val Glu
 20 25 30

agg aaa gag tgt gct tat tgc cta acc atc aac acc acc atc tgt gct 144
 Arg Lys Glu Cys Ala Tyr Cys Leu Thr Ile Asn Thr Thr Ile Cys Ala
 35 40 45

gga tat tgt atg aca cgg gat atc aat ggc aaa ctg ttt ctt ccc aaa 192

Gly Tyr Cys Met Thr Arg Asp Ile Asn Gly Lys Leu Phe Leu Pro Lys	
50 55 60	
tat gct ctg tcc caa gat gtt tgc acc tac aga gac ttc ctg tac aag	240
Tyr Ala Leu Ser Gln Asp Val Cys Thr Tyr Arg Asp Phe Leu Tyr Lys	
65 70 75 80	
act gta gaa ata cca gga tgc cca cac cat gtt act ccc tat ttc tcc	288
Thr Val Glu Ile Pro Gly Cys Pro His His Val Thr Pro Tyr Phe Ser	
85 90 95	
tac ccg gta gct gta agc tgt aaa tgt ggc aag tgt aat act gac tat	336
Tyr Pro Val Ala Val Ser Cys Lys Cys Gly Lys Cys Asn Thr Asp Tyr	
100 105 110	
agc gac tgc ata cat gag gcc atc aag aca aat gat tgt acc aaa ccc	384
Ser Asp Cys Ile His Glu Ala Ile Lys Thr Asn Asp Cys Thr Lys Pro	
115 120 125	
cag aag tcc gat gtg gta gga gtt tct atc taa	417
Gln Lys Ser Asp Val Val Gly Val Ser Ile	
130 135	

<210> 8
 <211> 835
 <212> DNA
 <213> Felis sp.

<400> 8

atgactgcta tctacctgat gtcctgtgctt tttggcctgg catgtggaca agcgatgtct	60
ttttgttttc caactgagta tatgatgcat gtcgaaagga aagagtgtgc ttattgccta	120
accatcaaca ccaccatctg tgetggatat tgtatgacac gggatatgtag ttcattctcac	180
ttcttttagc tgaaaattag ataaacctag actcagteca tttctatcca gaaaggaaat	240
gagataaatc acaacctcat ttcacagacc taacggtcac tggctcctta gaggtagagt	300
ccctagggtta taatatacgg acctactcca tacagttggt acagataatt tttacaatag	360
ttttactccc aaagtttatt taaaccttat ctgtgtccca cgatcaagga taaaagagag	420
gtgtgtgtgt atgtcatttt tttttgtctc tataggattc agtgtggata tgctgaattg	480
gtattgggga atgggactaa ggaatcctcc cccagtccta tttgtatcta tgggatgtaa	540
gcgaattaac attttgcttc ctcttctgtg cttccctcag gatatacatg gcaaactgtt	600
tcttcccaaa tatgctctgt cccaagatgt ttgcacctac agagacttcc tgtacaagac	660
tgtagaaata ccaggatgcc cacaccatgt tactccctat ttctcctacc cggtagctgt	720
aagctgtaaa tgtggcaagt gtaatactga ctatagcgac tgcatacatg aggccatcaa	780
gacaaatgat tgtaccaaac cccagaagtc cgatgtggta ggagtttcta tctaa	835

<210> 9
 <211> 360
 <212> DNA
 <213> Felis sp.

<400> 9

atggattact acagaaaata tgcagctgtc attctggcca tactctctgt gtttctgcat	60
attctccatt cttttcctga tggagagttt acaatgcagg ggtgccca atgcaagcta	120
aaggaaaaca aatacttctc caagttgggt gcccgaattt atcaatgcat gggctgctgc	180
ttctccagag catacccac tccagcaagg tccaagaaga caatgttggc cccaaagaac	240
atcacctcag aagccacatg ctgtgtggcc aaagccttta ccaaggccac ggtaatggga	300

aatgccaaaag tggagaatca cacagagtgc cactgcagca cttgctatca ccacaagatt 360

<210> 10

<211> 459

<212> DNA

<213> Felis sp.

<220>

<221> CDS

<222> (100)..(459)

<223> coding region for SEQ ID NO: 4

<220>

<221> CDS

<222> (172)..(459)

<223> coding region for SEQ ID NO: 3

<400> 10

agttactgag aaatcacaag acgaagccaa aatccctctt cagatccacg gtcaactgcc 60

ctgatcacat cctgcaaaaa gtccggagga aggagagcc atg gat tac tac aga 114
Met Asp Tyr Tyr Arg
1 5

aaa tat gca gct gtc att ctg gcc ata ctc tct gtg ttt ctg cat att 162
Lys Tyr Ala Ala Val Ile Leu Ala Ile Leu Ser Val Phe Leu His Ile
10 15 20

ctc cat tct ttt cct gat gga gag ttt aca atg cag ggg tgc cca gaa 210
Leu His Ser Phe Pro Asp Gly Glu Phe Thr Met Gln Gly Cys Pro Glu
25 30 35

tgc aag cta aag gaa aac aaa tac ttc tcc aag ttg ggt gcc cca att 258
Cys Lys Leu Lys Glu Asn Lys Tyr Phe Ser Lys Leu Gly Ala Pro Ile
40 45 50

tat caa tgc atg ggc tgc tgc ttc tcc aga gca tac ccc act cca gca 306
Tyr Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro Ala
55 60 65

agg tcc aag aag aca atg ttg gtc cca aag aac atc acc tca gaa gcc 354
Arg Ser Lys Lys Thr Met Leu Val Pro Lys Asn Ile Thr Ser Glu Ala
70 75 80 85

aca tgc tgt gtg gcc aaa gcc ttt acc aag gcc acg gta atg gga aat 402
Thr Cys Cys Val Ala Lys Ala Phe Thr Lys Ala Thr Val Met Gly Asn
90 95 100

gcc aaa gtg gag aat cac aca gag tgc cac tgc agc act tgc tat cac 450
Ala Lys Val Glu Asn His Thr Glu Cys His Cys Ser Thr Cys Tyr His
105 110 115

cac aag att 459
His Lys Ile
120

<210> 11
<211> 792
<212> DNA
<213> *Felis sp.*

<220>
<221> CDS
<222> (1)..(792)
<223> coding region for SEQ ID NO: 6

<220>
<221> CDS
<222> (61)..(792)
<223> coding region for SEQ ID NO: 5

<400> 11
atg act gct atc tac ctg atg tcc gtg ctt ttt ggc ctg gca tgt gga 48
Met Thr Ala Ile Tyr Leu Met Ser Val Leu Phe Gly Leu Ala Cys Gly
1 5 10 15

caa gcg atg tct ttt tgt ttt cca act gag tat atg atg cat gtc gaa 96
Gln Ala Met Ser Phe Cys Phe Pro Thr Glu Tyr Met Met His Val Glu
20 25 30

agg aaa gag tgt gct tat tgc cta acc atc aac acc acc atc tgt gct 144
Arg Lys Glu Cys Ala Tyr Cys Leu Thr Ile Asn Thr Thr Ile Cys Ala
35 40 45

gga tat tgt atg aca cgg gat atc aat ggc aaa ctg ttt ctt ccc aaa 192
Gly Tyr Cys Met Thr Arg Asp Ile Asn Gly Lys Leu Phe Leu Pro Lys
50 55 60

tat gct ctg tcc caa gat gtt tgc acc tac aga gac ttc ctg tac aag 240
Tyr Ala Leu Ser Gln Asp Val Cys Thr Tyr Arg Asp Phe Leu Tyr Lys
65 70 75 80

act gta gaa ata cca gga tgc cca cac cat gtt act ccc tat ttc tcc 288
Thr Val Glu Ile Pro Gly Cys Pro His His Val Thr Pro Tyr Phe Ser
85 90 95

tac ccg gta gct gta agc tgt aaa tgt ggc aag tgt aat act gac tat 336
Tyr Pro Val Ala Val Ser Cys Lys Cys Gly Lys Cys Asn Thr Asp Tyr
100 105 110

agc gac tgc ata cat gag gcc atc aag aca aat gat tgt acc aaa ccc 384
Ser Asp Cys Ile His Glu Ala Ile Lys Thr Asn Asp Cys Thr Lys Pro
115 120 125

cag aag tcc gat gtg gta gga gtt tct atc cag gac tcc tct tcc tca 432
Gln Lys Ser Asp Val Val Gly Val Ser Ile Gln Asp Ser Ser Ser Ser
130 135 140

aag gcc cct tcc gcc agc ctt cca agc cca acg cgt ctc ccg ggg ccc 480
Lys Ala Pro Ser Ala Ser Leu Pro Ser Pro Thr Arg Leu Pro Gly Pro
145 150 155 160

tcg gac acc ccg atc ctc cca caa ttt cct gat gga gag ttt aca atg 528

Ser Asp Thr Pro Ile Leu Pro Gln Phe Pro Asp Gly Glu Phe Thr Met
165 170 175

cag ggg tgc cca gaa tgc aag cta aag gaa aac aaa tac ttc tcc aag 576
Gln Gly Cys Pro Glu Cys Lys Leu Lys Glu Asn Lys Tyr Phe Ser Lys
180 185 190